

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/025,145

DATE: 01/15/2002

TIME: 18:55:54

Input Set : A:\18414seq.txt

Output Set: N:\CRF3\01152002\J025145.raw

6-7
Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Croteau, Rodney B
4 Bohlmann, Joerg
5 Steele, Christopher L
6 Phillips, Michael A
8 <120> TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
10 <130> FILE REFERENCE: WSUR18414
12 <140> CURRENT APPLICATION NUMBER: US/10/025,145
13 <141> CURRENT FILING DATE: 2001-12-19
15 <150> PRIOR APPLICATION NUMBER: 09/360,545
16 <151> PRIOR FILING DATE: 1999-07-26
18 <150> PRIOR APPLICATION NUMBER: 60/052,249
19 <151> PRIOR FILING DATE: 1997-07-11
21 <150> PRIOR APPLICATION NUMBER: PCT/US98/14528
22 <151> PRIOR FILING DATE: 1998-07-10
24 <160> NUMBER OF SEQ ID NOS: 107
26 <170> SOFTWARE: PatentIn Ver. 2.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 2196
30 <212> TYPE: DNA
31 <213> ORGANISM: Abies grandis
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (69)..(1952)
36 <223> OTHER INFORMATION: Clone AG2.2 encoding myrcene synthase
38 <400> SEQUENCE: 1
39 tgccggcagc aggttatctt gagcttcctc catataggcc aacacatatc atatcaaagg 60
41 gagcaaga atg gct ctg gtt tct atc tca ccg ttg gct tcg aaa tct tgc 110
42 Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys
43 1 5 10
45 ctg cgc aag tcg ttg atc agt tca att cat gaa cat aag cct ccc tat 158
46 Leu Arg Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr
47 15 20 25 30
49 aga aca atc cca aat ctt gga atg cgt agg cga ggg aaa tct gtc acg 206
50 Arg Thr Ile Pro Asn Leu Gly Met Arg Arg Arg Gly Lys Ser Val Thr
51 35 40 45
53 cct tcc atg agc atc agt ttg gcc acc gct gca cct gat gat ggt gta 254
54 Pro Ser Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val
55 50 55 60
57 caa aga cgc ata ggt gac tac cat tcc aat atc tgg gac gat gat ttc 302
58 Gln Arg Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe
59 65 70 75
61 ata cag tct cta tca acg cct tat ggg gaa ccc tct tac cag gaa cgt 350
62 Ile Gln Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg
63 80 85 90
65 gct gag aga tta att gtg gag gta aag aag ata ttc aat tca atg tac 398
66 Ala Glu Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr
67 95 100 105 110

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69 ctg gat gat gga aga tta atg agt tcc ttt aat gat ctc atg caa cgc 446
70 Leu Asp Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg
71      115      120      125
73 ctt tgg ata gtc gat agc gtt gaa cgt ttg ggg ata gct aga cat ttc 494
74 Leu Trp Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe
75      130      135      140
77 aag aac gag ata aca tca gct ctg gat tat gtt ttc cgt tac tgg gag 542
78 Lys Asn Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu
79      145      150      155
81 gaa aac ggc att gga tgt ggg aga gac agt att gtt act gat ctc aac 590
82 Glu Asn Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn
83      160      165      170
85 tca act gcg ttg ggg ttt cga act ctt cga tta cac ggg tac act gta 638
86 Ser Thr Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val
87 175      180      185      190
89 tct cca gag gtt tta aaa gct ttt caa gat caa aat gga cag ttt gta 686
90 Ser Pro Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val
91      195      200      205
93 tgc tcc ccc ggt cag aca gag ggt gag atc aga agc gtt ctt aac tta 734
94 Cys Ser Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu
95      210      215      220
97 tat cgg gct tcc ctc att gcc ttc cct ggt gag aaa gtt atg gaa gaa 782
98 Tyr Arg Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu
99      225      230      235
101 gct gaa atc ttc tcc aca aga tat ttg aaa gaa gct cta caa aag att 830
102 Ala Glu Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile
103      240      245      250
105 cca gtc tcc gct ctt tca caa gag ata aag ttt gtt atg gaa tat ggc 878
106 Pro Val Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly
107 255      260      265      270
109 tgg cac aca aat ttg cca aga ttg gaa gca aga aat tac ata gac aca 926
110 Trp His Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr
111      275      280      285
113 ctt gag aaa gac acc agt gca tgg ctc aat aaa aat gct ggg aag aag 974
114 Leu Glu Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys
115      290      295      300
117 ctt tta gaa ctt gca aaa ttg gag ttc aat ata ttt aac tcc tta caa 1022
118 Leu Leu Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln
119      305      310      315
121 caa aag gaa tta caa tat ctt ttg aga tgg tgg aaa gag tcg gat ttg 1070
122 Gln Lys Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu
123      320      325      330
125 cct aaa ttg aca ttt gct cgg cat cgt cat gtg gaa ttc tac act ttg 1118
126 Pro Lys Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu
127 335      340      345      350
129 gcc tct tgt att gcc att gac cca aaa cat tct gca ttc aga cta ggc 1166
130 Ala Ser Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly
131      355      360      365
133 ttc gcc aaa atg tgt cat ctt gtc aca gtt ttg gac gat att tac gac 1214

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134 Phe Ala Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp
135          370          375          380
137 act ttt gga acg att gac gag ctt gaa ctc ttc aca tct gca att aag 1262
138 Thr Phe Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys
139          385          390          395
141 aga tgg aat tca tca gag ata gaa cac ctt cca gaa tat atg aaa tgt 1310
142 Arg Trp Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys
143          400          405          410
145 gtg tac atg gtc gtg ttt gaa act gta aat gaa ctg aca cga gag gcg 1358
146 Val Tyr Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala
147 415          420          425          430
149 gag aag act caa ggg aga aac act ctc aac tat gtt cga aag gct tgg 1406
150 Glu Lys Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp
151          435          440          445
153 gag gct tat ttt gat tca tat atg gaa gaa gca aaa tgg atc tct aat 1454
154 Glu Ala Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn
155          450          455          460
157 ggt tat ctg cca atg ttt gaa gag tac cat gag aat ggg aaa gtg agc 1502
158 Gly Tyr Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser
159          465          470          475
161 tct gca tat cgc gta gca aca ttg caa ccc atc ctc act ttg aat gca 1550
162 Ser Ala Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala
163          480          485          490
165 tgg ctt cct gat tac atc ttg aag gga att gat ttt cca tcc agg ttc 1598
166 Trp Leu Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe
167 495          500          505          510
169 aat gat ttg gca tcg tcc ttc ctt cgg cta cga ggt gac aca cgc tgc 1646
170 Asn Asp Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys
171          515          520          525
173 tac aag gcc gat agg gat cgt ggt gaa gaa gct tcg tgt ata tca tgt 1694
174 Tyr Lys Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys
175          530          535          540
177 tat atg aaa gac aat cct gga tca acc gaa gaa gat gcc ctc aat cat 1742
178 Tyr Met Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His
179          545          550          555
181 atc aat gcc atg gtc aat gac ata atc aaa gaa tta aat tgg gaa ctt 1790
182 Ile Asn Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu
183          560          565          570
185 cta aga tcc aac gac aat att cca atg ctg gcc aag aaa cat gct ttt 1838
186 Leu Arg Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe
187 575          580          585          590
189 gac ata aca aga gct ctc cac cat ctc tac ata tat cga gat ggc ttt 1886
190 Asp Ile Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe
191          595          600          605
193 agt gtt gcc aac aag gaa aca aaa aaa ttg gtt atg gaa aca ctc ctt 1934
194 Ser Val Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu
195          610          615          620
197 gaa tct atg ctt ttt taa ctataaccat atccataata ataagctcat 1982
198 Glu Ser Met Leu Phe

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199          625
201 aatgctaaat tattggcctt atgacatagt ttatgtatgt acttgtgtga attcaatcat 2042
203 atcgtgtggg tatgattaaa aagctagagc ttactagggt agtaacatgg tgataaaagt 2102
205 tataaaatgt gagttataga gatacccatg ttgaataatg aattacaaaa agagaaattt 2162
207 atgtagaata agattggaag cttttcaatt gttt 2196
210 <210> SEQ ID NO: 2
211 <211> LENGTH: 627
212 <212> TYPE: PRT
213 <213> ORGANISM: Abies grandis
215 <400> SEQUENCE: 2
216 Met Ala Leu Val Ser Ile Ser Pro Leu Ala Ser Lys Ser Cys Leu Arg
217   1          5          10          15
219 Lys Ser Leu Ile Ser Ser Ile His Glu His Lys Pro Pro Tyr Arg Thr
220          20          25          30
222 Ile Pro Asn Leu Gly Met Arg Arg Gly Lys Ser Val Thr Pro Ser
223          35          40          45
225 Met Ser Ile Ser Leu Ala Thr Ala Ala Pro Asp Asp Gly Val Gln Arg
226          50          55          60
228 Arg Ile Gly Asp Tyr His Ser Asn Ile Trp Asp Asp Asp Phe Ile Gln
229  65          70          75          80
231 Ser Leu Ser Thr Pro Tyr Gly Glu Pro Ser Tyr Gln Glu Arg Ala Glu
232          85          90          95
234 Arg Leu Ile Val Glu Val Lys Lys Ile Phe Asn Ser Met Tyr Leu Asp
235          100         105         110
237 Asp Gly Arg Leu Met Ser Ser Phe Asn Asp Leu Met Gln Arg Leu Trp
238          115         120         125
240 Ile Val Asp Ser Val Glu Arg Leu Gly Ile Ala Arg His Phe Lys Asn
241          130         135         140
243 Glu Ile Thr Ser Ala Leu Asp Tyr Val Phe Arg Tyr Trp Glu Glu Asn
244 145          150         155         160
246 Gly Ile Gly Cys Gly Arg Asp Ser Ile Val Thr Asp Leu Asn Ser Thr
247          165         170         175
249 Ala Leu Gly Phe Arg Thr Leu Arg Leu His Gly Tyr Thr Val Ser Pro
250          180         185         190
252 Glu Val Leu Lys Ala Phe Gln Asp Gln Asn Gly Gln Phe Val Cys Ser
253          195         200         205
255 Pro Gly Gln Thr Glu Gly Glu Ile Arg Ser Val Leu Asn Leu Tyr Arg
256          210         215         220
258 Ala Ser Leu Ile Ala Phe Pro Gly Glu Lys Val Met Glu Glu Ala Glu
259 225          230         235         240
261 Ile Phe Ser Thr Arg Tyr Leu Lys Glu Ala Leu Gln Lys Ile Pro Val
262          245         250         255
264 Ser Ala Leu Ser Gln Glu Ile Lys Phe Val Met Glu Tyr Gly Trp His
265          260         265         270
267 Thr Asn Leu Pro Arg Leu Glu Ala Arg Asn Tyr Ile Asp Thr Leu Glu
268          275         280         285
270 Lys Asp Thr Ser Ala Trp Leu Asn Lys Asn Ala Gly Lys Lys Leu Leu
271          290         295         300
273 Glu Leu Ala Lys Leu Glu Phe Asn Ile Phe Asn Ser Leu Gln Gln Lys

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274 305          310          315          320
276 Glu Leu Gln Tyr Leu Leu Arg Trp Trp Lys Glu Ser Asp Leu Pro Lys
277          325          330          335
279 Leu Thr Phe Ala Arg His Arg His Val Glu Phe Tyr Thr Leu Ala Ser
280          340          345          350
282 Cys Ile Ala Ile Asp Pro Lys His Ser Ala Phe Arg Leu Gly Phe Ala
283          355          360          365
285 Lys Met Cys His Leu Val Thr Val Leu Asp Asp Ile Tyr Asp Thr Phe
286          370          375          380
288 Gly Thr Ile Asp Glu Leu Glu Leu Phe Thr Ser Ala Ile Lys Arg Trp
289 385          390          395          400
291 Asn Ser Ser Glu Ile Glu His Leu Pro Glu Tyr Met Lys Cys Val Tyr
292          405          410          415
294 Met Val Val Phe Glu Thr Val Asn Glu Leu Thr Arg Glu Ala Glu Lys
295          420          425          430
297 Thr Gln Gly Arg Asn Thr Leu Asn Tyr Val Arg Lys Ala Trp Glu Ala
298          435          440          445
300 Tyr Phe Asp Ser Tyr Met Glu Glu Ala Lys Trp Ile Ser Asn Gly Tyr
301          450          455          460
303 Leu Pro Met Phe Glu Glu Tyr His Glu Asn Gly Lys Val Ser Ser Ala
304 465          470          475          480
306 Tyr Arg Val Ala Thr Leu Gln Pro Ile Leu Thr Leu Asn Ala Trp Leu
307          485          490          495
309 Pro Asp Tyr Ile Leu Lys Gly Ile Asp Phe Pro Ser Arg Phe Asn Asp
310          500          505          510
312 Leu Ala Ser Ser Phe Leu Arg Leu Arg Gly Asp Thr Arg Cys Tyr Lys
313          515          520          525
315 Ala Asp Arg Asp Arg Gly Glu Glu Ala Ser Cys Ile Ser Cys Tyr Met
316          530          535          540
318 Lys Asp Asn Pro Gly Ser Thr Glu Glu Asp Ala Leu Asn His Ile Asn
319 545          550          555          560
321 Ala Met Val Asn Asp Ile Ile Lys Glu Leu Asn Trp Glu Leu Leu Arg
322          565          570          575
324 Ser Asn Asp Asn Ile Pro Met Leu Ala Lys Lys His Ala Phe Asp Ile
325          580          585          590
327 Thr Arg Ala Leu His His Leu Tyr Ile Tyr Arg Asp Gly Phe Ser Val
328          595          600          605
330 Ala Asn Lys Glu Thr Lys Lys Leu Val Met Glu Thr Leu Leu Glu Ser
331          610          615          620
333 Met Leu Phe
334 625
337 <210> SEQ ID NO: 3
338 <211> LENGTH: 2018
339 <212> TYPE: DNA
340 <213> ORGANISM: Abies grandis
342 <220> FEATURE:
343 <221> NAME/KEY: CDS
344 <222> LOCATION: (6)..(1892)
345 <223> OTHER INFORMATION: Clone AG3.18 encoding pinene synthase

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6

<210> : 11

<211> : 108

<212> DNA

<213>

Artificial Sequence

<220>

<223>

<400> : 11

gatgatgggt ttgatgcgca cggaacccta gatgaattga agctattcac tgaggctgtg 60
agaagatggg acctctcctt tacagacaac ttccccgatt acatgaaa 108

see item 11 on Eua Summary Sheet

PMI

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

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<210> 25
<211> 8
<212> PRT
<213> : Artificial Sequence

<220>
<223> : Description of Artificial Sequence: conserved

amino acid motif on which the sequence of Primer D

was based, wherein Xaa at position number 3 represents Thr or Ile, Xaa at

position number 4 represents Ile or Tyr or Phe, Xaa at position number 6

<2207> <2237> represents Ala or Val and Xaa at position number 8 represents Ala or Gly

Per 1.823 of Sequence Rules, 4 lines maximum
for <2237> response. Insert another <2207> after
4th line and insert a <2237> on 5th line.

IMPORTANT:

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:963 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1003 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1031 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1031 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1077 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1949 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2027 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:2058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2072 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2081 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:2102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2609 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45
L:2609 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45
L:2609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
L:2623 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2626 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
L:2626 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
L:2626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
L:2672 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2689 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2692 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:50
L:2692 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:50
L:2692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
L:2706 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2709 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:2709 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:2709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
L:2723 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2726 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:52
L:2726 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:52
L:2726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:2740 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:2743 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:53
L:2743 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:53
L:2743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
L:2786 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:56
L:2786 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:56
L:2786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56